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DATE: Tuesday, May 24, 2005

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☐	L2	L1 and (transgen$ or knockout or disrupt$ or delet$ or deficien$)	24
☐	L1	adenylate cyclase 7 or adcy7 or adcy 7	25

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NEWS 8 MAR 03 REGISTRY/ZREGISTRY - Sequence annotations enhanced
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NEWS 11 MAR 22 Original IDE display format returns to REGISTRY/ZREGISTRY
NEWS 12 MAR 22 PATDPASPC - New patent database available
NEWS 13 MAR 22 REGISTRY/ZREGISTRY enhanced with experimental property tags
NEWS 14 APR 04 EPFULL enhanced with additional patent information and new fields
NEWS 15 APR 04 EMBASE - Database reloaded and enhanced
NEWS 16 APR 18 New CAS Information Use Policies available online
NEWS 17 APR 25 Patent searching, including current-awareness alerts (SDIs), based on application date in CA/CAplus and USPATFULL/USPAT2 may be affected by a change in filing date for U.S. applications.
NEWS 18 APR 28 Improved searching of U.S. Patent Classifications for U.S. patent records in CA/CAplus
NEWS 19 MAY 23 GBFULL enhanced with patent drawing images
NEWS 20 MAY 23 REGISTRY has been enhanced with source information from CHEMCATS

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L3 ANSWER 1 OF 2 BIOSIS COPYRIGHT (c) 2005 The Thomson Corporation on STN
AN 2003:107195 BIOSIS
DN PREV200300107195
TI SIAH1 inactivation correlates with tumor progression in hepatocellular carcinomas.
AU Matsuo, Koichi [Reprint Author]; Satoh, Seiji; Okabe, Hiroshi; Nomura, Akinari; Maeda, Toshiki; Yamaoka, Yoshio; Ikai, Iwao
CS Department of Gastroenterological Surgery, Graduate School of Medicine, Kyoto University, 54 Kawahara-cho, Shogoin, Sakyo-ku, Kyoto, 606-8507, Japan
kmatsuo@kuhp.kyoto-u.ac.jp
SO Genes Chromosomes & Cancer, (March 2003) Vol. 36, No. 3, pp. 283-291. print.
CODEN: GCCAES. ISSN: 1045-2257.
DT Article
LA English
ED Entered STN: 26 Feb 2003
Last Updated on STN: 26 Feb 2003
AB Accumulation of loss of heterozygosity (LOH) on chromosome 16 is frequently observed in human hepatocellular carcinomas (HCCs). To identify tumor-suppressor genes (TSGs) involved in hepatocarcinogenesis, we performed ***deletion*** mapping of chromosome 16 in 59 HCCs. Three commonly ***deleted*** regions, located in 16q12.1, 16q22.1, and 16q24.2, were observed. Because there has been no study on LOH at locus 16q12.1 in HCCs, we focused on this region. By searching the Human Genome Database at the National Center for Biotechnology Information web site, we identified 14 known genes in 16q12.1 as TSG candidates. Among these, the expression of SIAH1 was markedly downregulated in HCCs, and inactivation of SIAH1 expression was associated with LOH at 16q12.1. A mutation analysis of SIAH1 revealed no somatic mutations, but one single nucleotide polymorphism was found among the 35 HCCs investigated. Subsequently, we evaluated the relation between SIAH1 expression, confirmed by semiquantitative RT-PCR, and clinicopathological parameters in HCCs. SIAH1 was significantly downregulated in advanced HCCs, including poorly differentiated tumors, larger tumors, and tumors in advanced stages. These findings suggest that inactivation of SIAH1 plays an important role in HCC progression.

L3 ANSWER 2 OF 2 CAPLUS COPYRIGHT 2005 ACS on STN
AN 2004:335782 CAPLUS
DN 140:401304
TI Nucleotide sequences useful in the identification of pharmaceutically active compounds
AU Martijn, Cecile; Johansson, Per; Sjoegren, Annelie; Walum, Erik; Lind, Peter; Enerbaeck, Sven; Rondahl, Lena
CS Biovitrum AB, UK
SO Research Disclosure (2003), Volume Date 2004, 477(Jan.), P23-P24 (No. 477015)
CODEN: RSDSBB; ISSN: 0374-4353
PB Kenneth Mason Publications Ltd.
DT Journal; Patent
LA English

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI RD 477015		20040110		
PRAI RD 2004-477015		20040110		

AB Nucleotide sequences that are predicted to be useful in methods for identification of pharmaceutically active compds. are presented. Such compds. are predicted to be useful for the treatment or prophylaxis of metabolic diseases, such as obesity and type 2 diabetes.

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